

```

1  MAPGWPRSLPQILVLGLFGLVLMRAAAGEQAPGTSPCSSGSSWSADLDKCM 50
   || | | |.:||| | |:|. ||||| |. ||||| ||||| |||||
1  MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCM 50
   . . . . .
51 DCASCPARPHSDFCLGCAAAPPAHFRLLWPILGGALSLVLVLALVSSFLV 100
   ||||| ||||| ||||| ||||| ||||| ||||| |||. |||||
51 DCASCRARPHSDFCLGCAAAPPAFRLLWPILGGALSLTFVLGLLSGFLV 100
   . . .
101 WRRCRRREKFTTPIEETGGEGCPGVALIQ 129
   ||||| ||||| ||||| ||||| |||||
101 WRRCRRREKFTTPIEETGGEGCPAVALIQ 129

```

Fig. 1

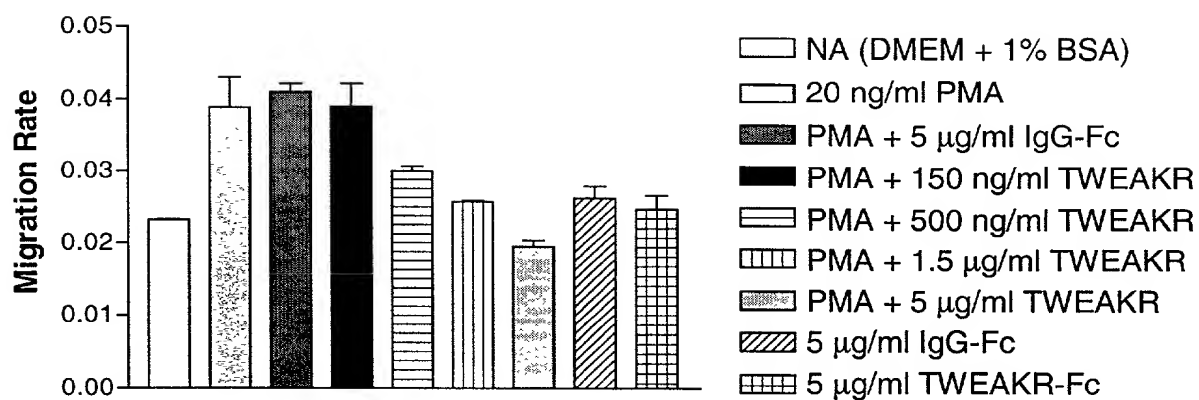


Fig. 2

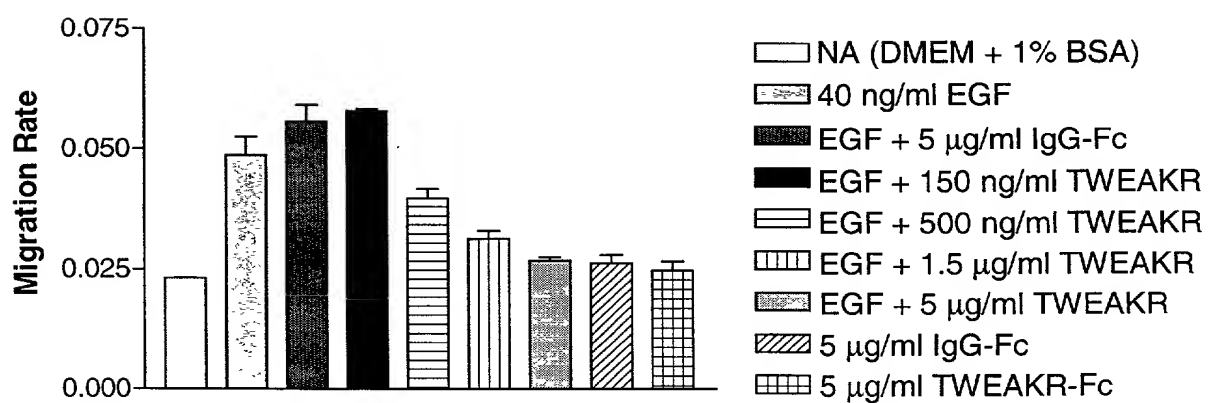


Fig. 3

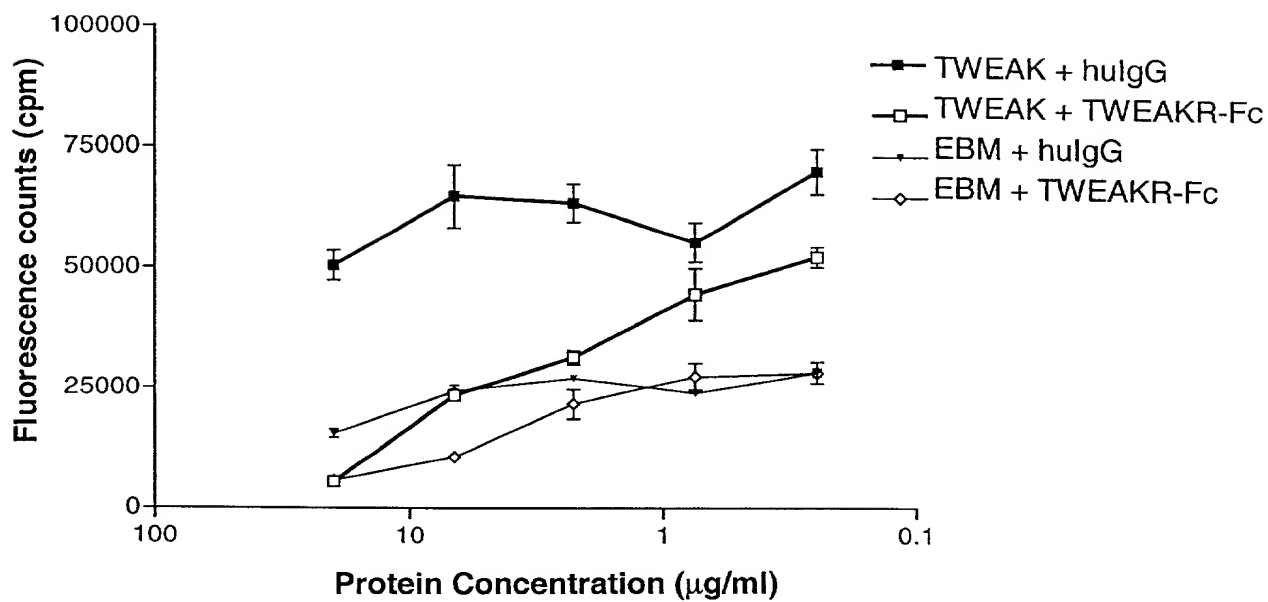


Fig. 4

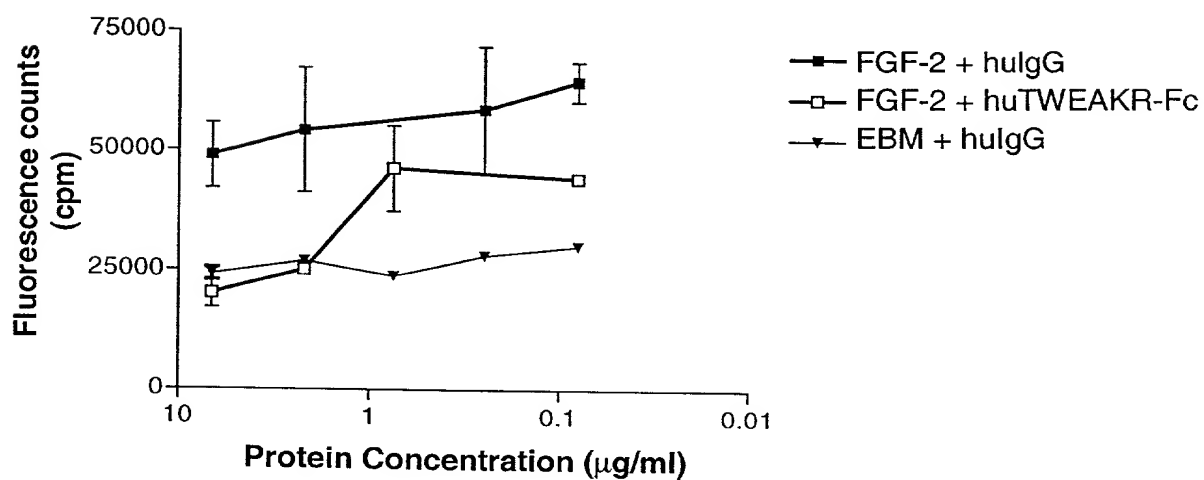


Fig. 5